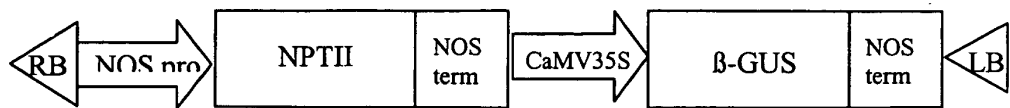
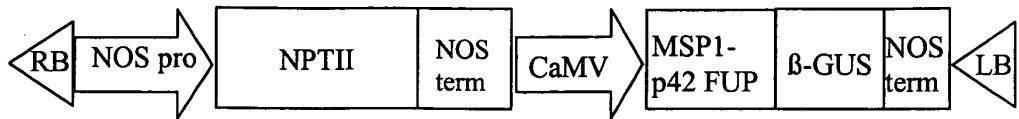


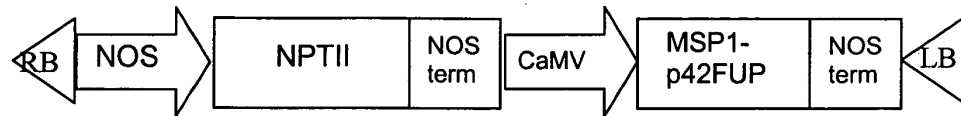
**Fig. 1(A)**



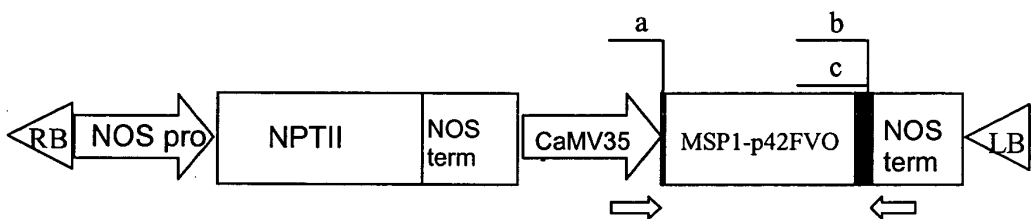
**Fig. 1(B)**

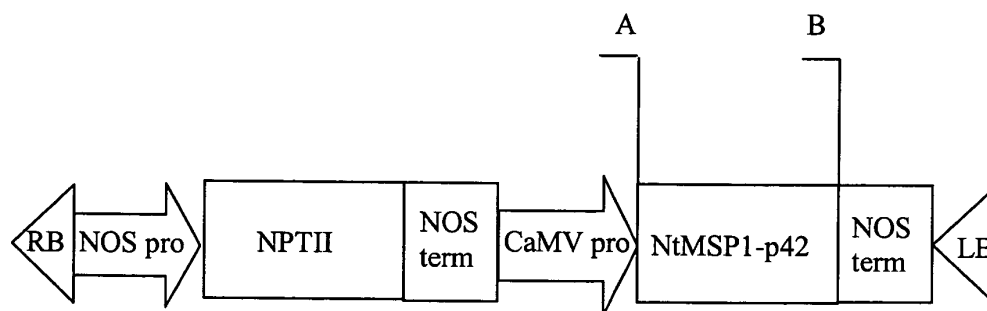


**Fig. 1(C)**

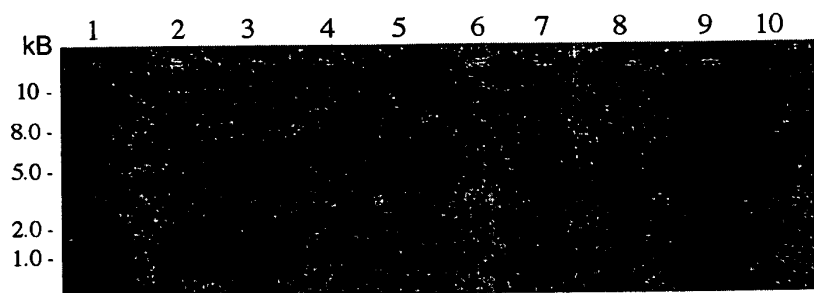


**Fig. 1(D)**

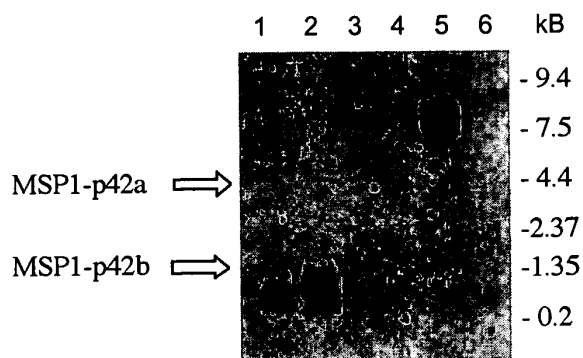




**Fig. 2**



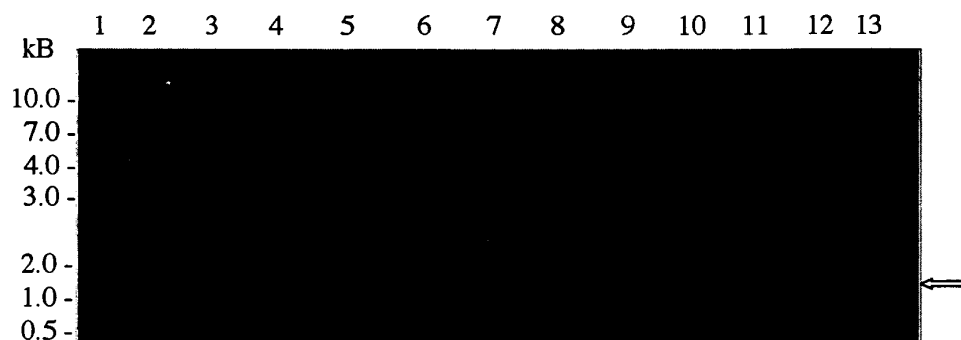
**Fig. 3(A)**



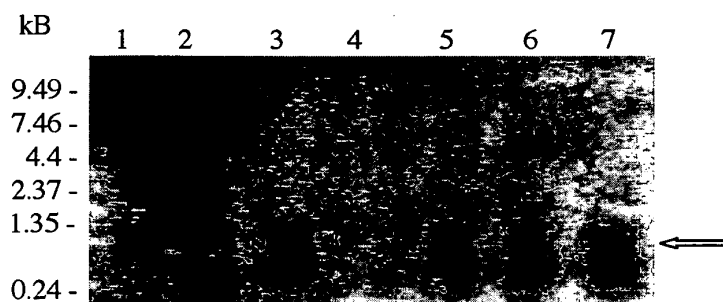
**Fig. 3(B)**

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**Fig 4(A)**

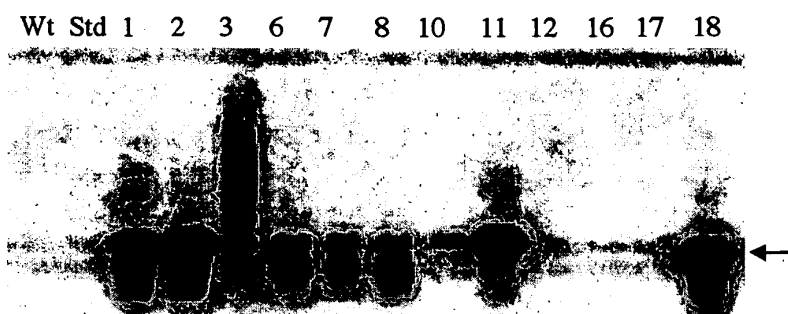


**Fig. 4(B)**

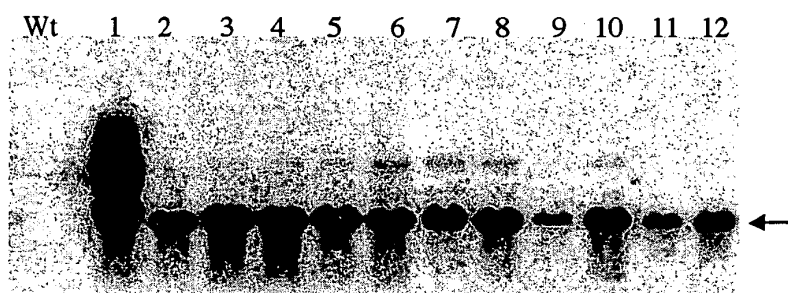


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**Fig. 5(A)**

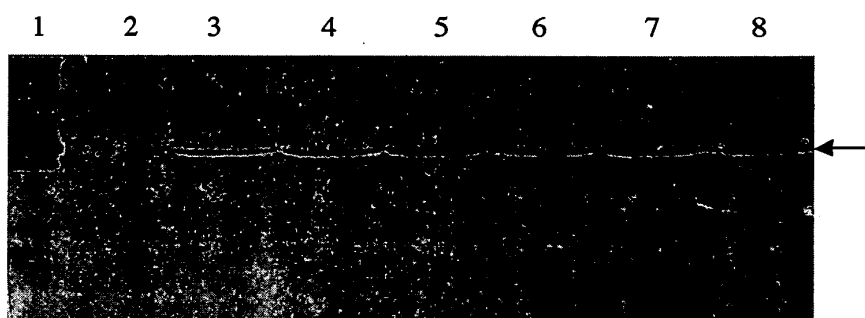
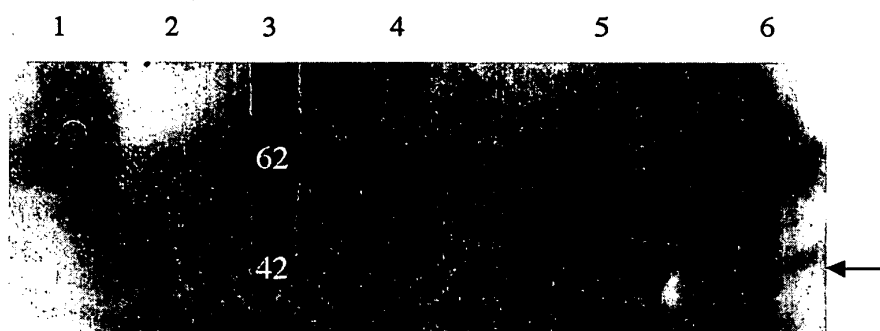


**Fig. 5(B)**



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**Fig 6(A)**



**Fig. 6(B)**

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[illegible]

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601 AACATTGAGAC CTTATACAATAAC TTAGTT**AATAAAAT** TGACGATTACTT  
951 TCCAGAAAAT TCTGGATGTTTCAGAC ATTTAGATGAAAG AGAAGAATGTA

181 AATTTCAAAATG TTTTAGAATCAGATTTA ATTCCATATAAAG ATTTA  
230 ACATCAAGTAATT ATGTTGTCAAAGATCCA TATAAATTTCTTA**AATAAA**  
277 GAAAAAAGAGA TAAATTCTTAAGCAGTTA TAATTATATTAAGGATTC

**Fig. 7(B)**





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R I Q G D I T M D N I L S G F E N E	18
CGG ATC CAA GGA GAT ATA ACA ATG GAC AAC ATC CTC AGT GGC TTC GAG AAC GAG	54
Y D V I Y L K P L A G V Y R S L K K	36
TAC GAC GTA ATC TAC CTA AAG CCC CTT GCC GGT GTC TAC CGT TCA TTG AAG AAA	108
Q I E K N I F T F N L N L N D I L N	54
CAG ATA GAA AAG AAT ATT TTC ACG TTC AAC CTC AAC CTA AAT GAC ATC CTC AAC	162
S R L K K R K Y F L D V L E S D L M	72
TCG CGC CTC AAG AAG CGA AAA TAC TTC CTC GAC GTG TTG GAA TCC GAC CTT ATG	216
Q F K H I S S N E Y I I E D S F K L	90
CAA TTC AAG CAC ATT AGC TCT AAC GAG TAC ATC ATA GAG GAC AGC TTC AAG CTC	270
L N S E Q K N T L L K S Y K Y I K E	108
TTG AAT TCA GAA CAG AAG AAC ACC CTC CTA AAG TCC TAC AAA TAC ATT AAG GAG	324
S V E N D I K F A Q E G I S Y Y E K	126
TCT GTT GAG AAC GAC ATC AAG TTC GCC CAG GAA GGA ATT AGC TAC TAT GAG AAA	378
V L A K Y K D D L E S I K K V I K E	144
GTC CTG GCT AAA TAC AAG GAC GAC TTG GAA AGC ATT AAG AAG GTA ATC AAA GAA	432
E K E K F P S S P P T T P P S P A K	162
GAG AAG GAA AAG TTT CCG AGC TCT CCA CCC ACA ACT CCC CCA TCG CCT GCA AAG	486
T D E Q K K E S K F L P F L T N I E	180
ACC GAC GAG CAG AAA AAA GAA AGT AAG TTC CTT CCA TTC CTC ACC AAC ATC GAA	540
T L Y N N L V N K I D D Y L I N L K	198
ACT CTA TAT AAC AAC CTG GTG AAC AAG ATT GAT GAC TAC TTA ATC AAC TTG AAG	594
A K I N D C N V E K D E A H V K I T	216
GCG AAA ATT AAT GAC TGT AAC GTC GAA AAG GAT GAA GCC CAC GTT AAG ATC ACC	648
K L S D L K A I D D K I D L F K N H	234
AAG CTT TCC GAT CTC AAA GCC ATC GAC GAT AAG ATT GAC CTG TTT AAG AAC CAC	702
N D F D A I K K L I N D D T K K D M	252
AAC GAT TTC GAC GCA ATC AAA AAG TTG ATC AAC GAC GAT ACT AAG AAA GAC ATG	756
L G K L L S T G L V Q N F P N T I I	270
CTT GGA AAA CTG CTG TCG ACA GGC TTG GTC CAA AAC TTC CCG AAC ACC ATT ATA	810
S K L I E G K F Q D M L N I S Q H Q	288
AGC AAG CTG ATC GAA GGA AAG TTT CAG GAT ATG CTG AAC ATC TCT CAG CAT CAA	864
C V K K Q C P E N S G C F R H L D E	306
TGC GTG AAG AAG CAA TGT CCC GAG AAT TCA GGT TGC TTC CGC CAC TTA GAC GAA	918
R E E C K C L L N Y K Q E G D K C V	324
AGG GAG GAA TGT AAA TGC CTG CTG AAT TAT AAA CAG GAA GGA GAC AAG TGC GTA	972
E N P N P T C N E N N G G C D A D A	342
GAG AAT CCT AAC CCA ACC TGT AAC GAA AAT AAC GGT GGC TGC GAT GCT GAC GCT	1026
K C T E E D S G S N G K K I T C E C	360
AAG TGT ACC GAG GAG GAC AGC GGT TCC AAT GGC AAG AAA ATA ACT TGC GAA TGC	1080
T K P D S Y P L F D G I F C S H D E	378
ACG AAG CCC GAT AGT TAC CCT CTC TTC GAC GGT ATC TTC TGC TCC CAT GAT GAG	1134
L * E L T	383
CTT TAA GAG CTC ACC	1149

Fig 9

# Fig 10

## DNA AND AMINO ACID SEQUENCE OF BVp42-M

attggatccactaaa

13 atgtggtccttggaagtgtcttttattctgggctgtccttggtgacc  
M W S W K C L L F W A V L V T  
58 gccactctttgcacagcagcgatctctgttactatggacaacatc  
A T L C T A A I S V T M D N I  
103 ctcagtggcttcgagaacgagtagcagcgtaatctacctaagccc  
L S G F E N E Y D V I Y L K P  
148 cttgccggtgtctaccgttcattgaagaaacagatagaaaagaat  
L A G V Y R S L K K Q I E K N  
193 attttcacgttcaacctcaacctaaatgacatcctcaactcgcgc  
I F T F N L N L N D I L N S R  
238 ctcaagaagcgaaaatacttcctcgacgtgttggaatccgacctt  
L K K R K Y F L D V L E S D L  
283 atgcaatttaagcacattagctctaacgagtagcatcatagaggac  
M Q F K H I S S N E Y I I E D  
328 agcttcaagctcttgaattcagaacagaagaacaccctcctaag  
S F K L L N S E Q K N T L L K  
373 tcctacaaatacattaaggagtctgttgagaacgacatcaagttc  
S Y K Y I K E S V E N D I K F  
418 gccaggaaggaattagctactatgagaaagtcctggctaataac  
A Q E G I S Y Y E K V L A K Y  
463 aaggacgacttggaagcattaagaaggtaatcaaagaagagaag  
K D D L E S I K K V I K E E K  
508 gaaaagtttccgagctctccaccacaactccccatcgctgca  
E K F P S S P P T T P P S P A  
553 aagaccgacgagcagaaaaaagaaagtaagttccttcattcctc  
K T D E Q K K E S K F L P F L  
598 accaacatcgaaactctatataacaacctggtgaacaagattgat  
T N I E T L Y N N L V N K I D  
643 gactacttaatcaacttgaaggcgaaaattaatgactgtaacgtc  
D Y L I N L K A K I N D C N V  
688 gaaaaggatgaagcccacgttaagatcaccaagctttccgatctc  
E K D E A H V K I T K L S D L  
733 aaagccatcgacgataagattgacctgtttaagaaccacaacgat  
K A I D D K I D L F K N H N D  
778 ttcgacgcaatcaaaaagttgatcaacgacgataactaagaaagac  
F D A I K K L I N D D T K K D  
823 atgcttgaaaaactgctgtcgacaggcttgggtccaaaacttccc  
M L G K L L S T G L V Q N F P  
868 aacaccattataagcaagctgatcgaaggaaagtttcaggatatg

100954.031102

N T I I S K L I E G K F Q D M  
 913 ctgaacatctctcagcatcaatgcgtgaagaagcaatgtcccgag  
 L N I S Q H Q C V K K Q C P E  
 958 aattcagggttgcttccgccacttagacgaaagggaggaatgtaaa  
 N S G C F R H L D E R E E C K  
 1003 tgcctgctgaattataaacaggaaggagacaagtgcgtagagaat  
 C L L N Y K Q E G D K C V E N  
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 T C E C T K P D S Y P L F D G  
 1183 atcttctgctcc  
 I F C S

ccacctcatcatcatcatcattaataaggtaccta  
 P P H H H H H H \* \*

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